

FIG. 1

FIG. 2a

FIG. 2

GGT GAA GAA GGA GTT GTG CCA GCA CGT GAG TAC TCA GAC GAT CGT 45
Gly Glu Glu Gly Val Val Pro Ala Arg Glu Tyr Ser Asp Asp Arg [15]

AAC ATC AAC CTG GCA GAC GAA TTA AAA ATT GGT GAT ACC ATT GAA 90
Asn Ile Asn Leu Ala Asp Glu Leu Lys Ile Gly Asp Thr Ile Glu [30]

GCA GTT GTC ATT TCT AAC GTA ACA AGC GAC AAG GAA GCC GTC AGT 135
Ala Val Val Ile Ser Asn Val Thr Ser Asp Lys Glu Gly Val Ser [45]

TAC TTG TTG TCA AAG AAG CGT TTG GAT GCG CGC AAG GCA TGG GAA 180
Tyr Leu Leu Ser Lys Lys Arg Leu Asp Ala Arg Lys Ala Thr Glu [60]

AAC TTG AGC TTT GCT GAA GGT GAC ACAGTT GAT GCC AAG GTT ATC 225
Asn Leu Ser Phe Ala Glu Gly Asp Thr Val Asp Ala Lys Val Ile [75]

AAC GCT GTT CGT GGT TTG ATT GTT GAT GTT AAC GCC GTA CGT 270
Asn Ala Val Arg Gly Gly Leu Ile Val Asp Val Asn Gly Val Arg [90]

GGT TTC GTA CCA GCA TCA ATG GTT GCA GAA CGT TTC GTT TCT GAT 315
Gly Phe Val Pro Ala Ser Met Val Ala Glu Arg Phe Val Ser Asp [105]

TTG-AAC CAA TTC AAG AAT AAG GAT ATT AAA GCA CAA GTT ATC GAA 360
Leu Asn Gln Phe Lys Asn Lys Asp Ile Lys Ala Gln Val Ile Glu [120]

ATT GAC CCT GCT AAT GCA CGT TTG ATT TTG TCA CGT AAG GCT GTT 405
Ile Asp Pro Ala Asn Ala Arg Leu Ile Leu Ser Arg Lys Ala Val [135]

GCT GCA CAA GAA CGC GCT GCA CGA TTG GCT GAA GTA TTT AGC AAG 450
Ala Ala Gln Glu Arg Ala Ala Gln Leu Ala Glu Val Phe Ser Lys [150]

TTG TCA GTT CGT GAA GTT GTT GAA GGA ACT GTT GCC CGT TTG ACA 495
Leu Ser Val Gly Glu Val Val Glu Gly Thr Val Ala Arg Leu Thr [165]

GAC TTC GGC GCA TTC GTT GAC TTG GGT GGT GTT GAT GGT TTG GTT 540
Asp Phe Gly Ala Phe Val Asp Leu Gly Gly Val Asp Gly Leu Val [180]

CAC GTA TCA GAA ATC TCA CAC GAT CGT GTG AAG AAC CCG GCC GAT 585
His Val Ser Glu Ile Ser His Asp Arg Val Lys Asn Pro Ala Asp [195]

GTA TTG ACA AAG GGT GAC AAG GTT GAT GTT AAG ATC TTG GCA TTG 630
Val Leu Thr Lys Gly Asp Lys Val Asp Val Lys Ile Leu Ala Leu [210]

GAC ACT GAA AAG GGT CGT ATC TCA TTG TCA ATC AAA GCA ACA CAA 675
Asp Thr Glu Lys Gly Arg Ile Ser Leu Ser Ile Lys Ala Thr Gln [225]

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FIG. 2b

~~FIG. 2a~~

CGT GGA CCT TGG GAC GAA GCT GCA GAT CAA ATC GCT GCA GGT TCA 720
Arg Gly Pro Trp Asp Glu Ala Ala Asp Gln Ile Ala Ala Gly Ser [240]

GTC CTT GAA GGT ACT GTT AAG CGT GTG AAG GAC TTT GGT GCC TTT 765
Val Leu Glu Gly Thr Val Lys Arg Val Lys Asp Phe Gly Ala Phe [255]

GTT GAA ATT TTG CCT GGT ATC GAA GGT CTT GTG CAC GTG TCA CAA 810
Val Glu Ile Leu Pro Gly Ile Glu Gly Leu Val His Val Ser Gln [270]

ATT TCA AAC AAG CGT ATT GAA AAC CCA TCA GAA GTT TTG AAG TCT 855
Ile Ser Asn Lys Arg Ile Glu Asn Pro Ser Glu Val Leu Lys Ser [285]

GGT GAC AAG GTA CAA GTG AAG GTA TTG GAC ATT AAG CCA GCC GAA 900
Gly Asp Lys Val Gln Val Lys Val Leu Asp Ile Lys Pro Ala Glu [300]

GAA CGT ATT TCA TTG TCA ATG AAG GCT TTG GAA GAA AAG CCA GAA 945
Glu Arg Ile Ser Leu Ser Met Lys Ala Leu Glu Glu Lys Pro Glu [315]

CGT GAA GAT CGT CGT GGT AAC GAT GGT TCA GCT TCA CGT GCT GAT 990
Arg Glu Asp Arg Arg Gly Asn Asp Gly Ser Ala Ser Arg Ala Asp [330]

ATC GCT GCT TAC AAG CAA CAA GAT GAC TCA GCC GCA ACA TTG GGT 1035
Ile Ala Ala Tyr Lys Gln Gln Asp Asp Ser Ala Ala Thr Leu Gly [345]

GAC ATC TTT GGT GAT AAG TTG TAA GAGGCATCACATAAAAGAGCTGGTTC 1086
Asp Ile Phe Gly Asp Lys Leu *** [352]

GCCAGTTCTTTATTTGAAGAAAATTGAGTGGCATTAGTGGCGCTCACGGTATG 1145

AAAAAGGAGGTGGCATTATGGCAGCACCAGTAGTAGCCATTGTTGGCGACCAAACGTCG 1204

GAAAATCGACTATCTTAACCGGATGGCCGGAGAACGTATTGCAATGTTGAAGATCAA 1263

CCAGGGTAACACCGCATCGTTGACCGCCAGCCGATGGTTGAATTAT 1314

PROTEIN SEQUENCE

~~F/G.~~ ~~3a.~~

HS1	63	SFAEGDTVDKMINAVRGGLIVLDYNGVRGFPASMVAAERFVSDLNOFKNKDIKAQVIEI	121
ES1	101	AYEDAE--TGIVNGK-K--FT-ELD -A-L-G-L- DV-P-R -TLHLEG-ELEFK-- KL	159
RS1	107	K-EA-ER-EGI IF-Q-K- -FT- -LD-AVA -R-Q- DI- PIR- VTPADAQPAAALRNK I KM	165
PS1	1	E- -TGIVNGK-K- -FT- EL- -I- A- L- G-L- DV-P-R -TLHLEG -ELEFK- -- KL	54
CS1	182	- DVI-XKG-IVG-NK- -VVAI-E-L- --- F-Q- SSK- -SAEEL E-PLKFV - V	236
		a b c	
		*****	*****
HS1	122	D PANARLILSRKAVAAQERAQLAEVFSKL SYGEVVEGTIVARLTDFGAFVDLGGV D GLV	180
ES1	160	-QRNNWAV-R- -IES - NS- -ERDQLEN-QE- ME-K- I-KN- -Y----- -----L	218
RS1	166	-KRAGNIIV- -RT- -LEES - -E- -RS-IVQN -EE- Q- -V-KN- -Y----- -----L	224
PS1	55	-QRKRNNWAV-R- -IES - SS- -ERDQLEN -QE-ME-K- I-KN- -Y----- -----L	113
CS1	237	-EEQS--VM-NRKAM-DSQ- M- DSOAQ-GI- S---T- -QS-KPY- -I- - N - -L	287
		d e	
		*****	*****
HS1	181	H VSEI SHDRVKNPADVLTKGD KV D K V D K I L A D T E K R I S L I K A T Q R G P W D E A A D Q I A A G	239
ES1	219	-ITDMAWK- -H-SEIVNV - -E IT - -V-KF-R- RT -V- -GL-QLGED- -VAI- KRYPE-	277
RS1	225	-ITDMAWR- -H-SEIQNI - -QQ-K- Q- IRINQ. TH --- -GM-QLES D---GIGAKYPV-	283
PS1	114	-ITDMAWK- -H-SEIVNV - -E IT - -V-KF-R- RT -V- -GL-QLGED- -VAI- KRYPE-	172
CS1	288	--Q- -SDI- T- -QP- - TLK - M- SH- R- R- V- - -T- K- LEPT - G-	337
		d e	
		*****	*****

PROGETTO: SETTEZZO

EZG. 36

FIG. 3a

HS1 240 SVILEGTYKAVKDGFVELLPGEGLVHVSQISNKRNIENPSEVKSGDVKQVRYLDIKP 298
ES1 278 TK-T-R-TNLT-Y-C ---EE-V-----EM RD-V-DATL-SV --E-EA-FTGVDR 510
RS1 284 KRS ---TNLT-Y-----LE-----I-I-EM -RPG-QVI-EFNK --V-RAV---YDV 430
PS1 173 TK-T-R-TNLT-Y-C ---EE-V-----EM -K --E JAAV --QVDA 319

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HS1 299 AERISLSMKALEEKPERE 317
ES1 511 KNR-----VR-KD-AD-KD 529
RS1 431 DK -----GI-QL 442
PS1 320 ER -----GV-QLA-DP 335

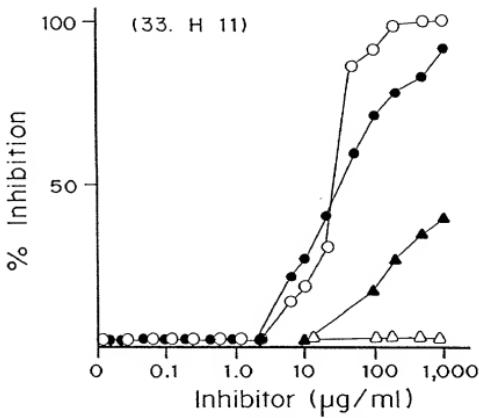


FIG. 4a

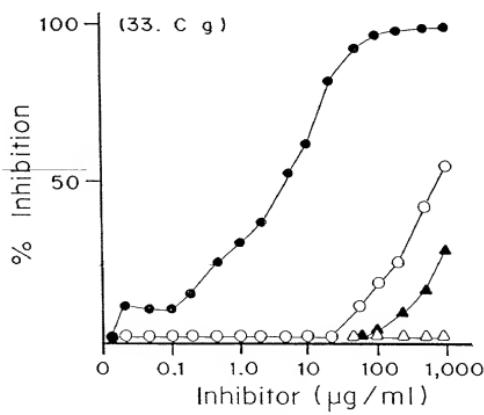


FIG. 4b

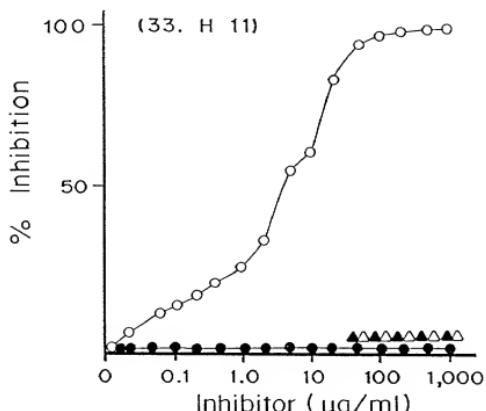


FIG. 4c

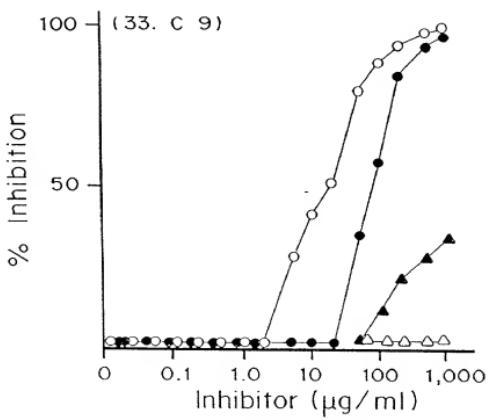


FIG. 4d